



IFWO

## RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/777,789

TIME: 14:51:54

Input Set : N:\Crf3\RULE60\10777789.raw.txt

Output Set: N:\CRF4\08302004\J777789.raw

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1 <110> APPLICANT: Oppmann, Birgit
2   Timans, Jacqueline C.
3   Kastelein, Robert A.
4   Bazan, J. Fernando
5 <120> TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
6 <130> FILE REFERENCE: DX0935K
7 <140> CURRENT APPLICATION NUMBER: US/10/777,789
8 <141> CURRENT FILING DATE: 2004-02-11
9 <150> PRIOR APPLICATION NUMBER: US/09/521,335
10 <151> PRIOR FILING DATE: 2000-03-09
11 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 1790
16 <212> TYPE: DNA
17 <213> ORGANISM: primate
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (162)..(806)
21 <220> FEATURE:
22 <221> NAME/KEY: mat_peptide
23 <222> LOCATION: (213)..(806)
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25   ccgagcga aaaacctg agtgggctg gcggatggga ttattaaagc ttcgccggag 60
26   ccgcggtcgc cctcccact ccgccagcct ccgggagagg agccgcaccc ggccggcccg 120
27   gcccagccc catggacctc cgagcagggg actcgtgggg g atg tta gcg tgc ctg 176
28                                     Met Leu Ala Cys Leu
29                                     -15
30   tgc acg gtg ctc tgg cac ctc cct gca gtg cca gct ctc aat cgc aca 224
31   Cys Thr Val Leu Trp His Leu Pro Ala Val Pro Ala Leu Asn Arg Thr
32   -10 -5 -1 1
33   ggg gac cca ggg cct ggc ccc tcc atc cag aaa acc tat gac ctc acc 272
34   Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys Thr Tyr Asp Leu Thr
35   5 10 15 20
36   cgc tac ctg gag cac caa ctc cgc agc ttg gct ggg acc tat ctg aac 320
37   Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala Gly Thr Tyr Leu Asn
38   25 30 35
39   tac ctg ggc ccc cct ttc aac gag cca gac ttc aac cct ccc cgc ctg 368
40   Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe Asn Pro Pro Arg Leu
41   40 45 50
42   ggg gca gag act ctg ccc agg gcc act gtt gac ttg gag gtg tgg cga 416
43   Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp Leu Glu Val Trp Arg
44   55 60 65

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45      agc ctc aat gac aaa ctg cgg ctg acc cag aac tac gag gcc tac agc      464
46      Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn Tyr Glu Ala Tyr Ser
47          70                      75                      80
48      cac ctt ctg tgt tac ttg cgt ggc ctc aac cgt cag gct gcc act gct      512
49      His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg Gln Ala Ala Thr Ala
50          85                      90                      95                      100
51      gag ctg cgc cgc agc ctg gcc cac ttc tgc acc agc ctc cag gcc ctg      560
52      Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr Ser Leu Gln Gly Leu
53          105                      110                      115
54      ctg ggc agc att gcg ggc gtc atg gca gct ctg ggc tac cca ctg ccc      608
55      Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu Gly Tyr Pro Leu Pro
56          120                      125                      130
57      cag ccg ctg cct ggg act gaa ccc act tgg act cct ggc cct gcc cac      656
58      Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr Pro Gly Pro Ala His
59          135                      140                      145
60      agt gac ttc ctc cag aag atg gac gac ttc tgg ctg ctg aag gag ctg      704
61      Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp Leu Leu Lys Glu Leu
62          150                      155                      160
63      cag acc tgg ctg tgg cgc tcg gcc aag gac ttc aac cgg ctc aag aag      752
64      Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe Asn Arg Leu Lys Lys
65          165                      170                      175                      180
66      aag atg cag cct cca gca gct gca gtc acc ctg cac ctg ggg gct cat      800
67      Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu His Leu Gly Ala His
68          185                      190                      195
69      ggc ttc tgacttctga ccttctcctc ttcgctcccc cttcaaacc cttctccact      856
70      Gly Phe
71
72      ttgtgagagc cagccctgta tgccaacacc tgttgagcca ggagacagaa gctgtgagcc 916
73      tctggccctt tccctggaccg gctgggctgt tgatgcgac agccctgtct cctccccacc 976
74      tcccaaaggc ctaccgagct ggggaggagg tacagtaggc cctgtcctgt cctgtttcta 1036
75      caggaagtca tgctcgaggc agtgtgaagt gggtcaggtt ggtgcagagg cgctcatggc 1096
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77      gagggcaggg gttgaggggc caccaccaca catgcctttc tggggtgaag ccctttggct 1216
78      gccccactct ccttggtatg gtgttgctcc cttatcccca aatcactcta tacatccaat 1276
79      tcaggaaaca aacatggtgg caattctaca caaaaagaga tgagattaac agtgcagggc 1336
80      tggggtctgc attggagggt ccctataaac cagaagagaa aatactgaaa gcacaggggc 1396
81      agggacagac cagaccagac ccaggagtct ccaaagcaca gaggggcaaa caaaacccga 1456
82      gctgagcatc aggaccttgc ctgcaattgt cttccagtat tacggtgcct cttctctgcc 1516
83      ccctttccca ggggtatctgt ggggttgccag gctggggagg gcaaccatag ccacaccaca 1576
84      ggatttcctg aaagtttaca atgcagtagc attttggggg taggggtggc agctccccc 1636
85      ggcctgccc ccagcccca cccactcatg actctaagtg tgttgattta atatttattt 1696
86      atttgagat gttatttatt agatgatatt tattgcagaa tttctattct tgtattaaca 1756
87      aataaaatgc ttgccccaga acaaaaaaaaa aaaa 1790
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 215
91 <212> TYPE: PRT
92 <213> ORGANISM: primate
93 <400> SEQUENCE: 2
94      Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
95          -15                      -10                      -5

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96      Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
97      -1   1           5           10           15
98      Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
99              20           25           30
100     Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
101              35           40           45
102     Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp
103              50           55           60
104     Leu Glu Val Trp Arg Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn
105              65           70           75
106     Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
107              80           85           90           95
108     Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
109              100          105          110
110     Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu
111              115          120          125
112     Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr
113              130          135          140
114     Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
115              145          150          155
116     Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
117              160          165          170          175
118     Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu
119              180          185          190
120     His Leu Gly Ala His Gly Phe
121              195
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124 <211> LENGTH: 648
125 <212> TYPE: DNA
126 <213> ORGANISM: primate
127 <220> FEATURE:
128 <221> NAME/KEY: CDS
129 <222> LOCATION: (1)..(645)
130 <220> FEATURE:
131 <221> NAME/KEY: mat_peptide
132 <222> LOCATION: (52)..(645)
133 <400> SEQUENCE: 3
134     atg tta gct tgc cta tgc acg gtg ctg tgg cac ctc cct gca gtg cca 48
135     Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
136             -15             -10             -5
137     gct ctt aat cgc aca gga gat cca ggc cct ggc ccc tcc atc cag aaa 96
138     Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
139     -1   1           5           10           15
140     acc tat gac ctc acc cgc tac ctg gag cat caa ctc cgc agc tta gct 144
141     Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
142             20           25           30
143     ggg acc tac ctg aac tac ctg ggg ccc cct ttc aac gag cct gac ttc 192
144     Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
145             35           40           45

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146 aat cct cct cga ctg ggg gca gaa act ctg ccc agg gcc acg gtc aac 240
147 Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
148      50      55      60
149 ttg gaa gtg tgg cga agc ctc aat gac agg ctg cgg ctg acc cag aac 288
150 Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
151      65      70      75
152 tat gag gcg tac agt cac ctc ctg tgt tac ttg cgt ggc ctc aac cgt 336
153 Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
154      80      85      90      95
155 cag gct gcc aca gct gaa ctc cga cgt agc ctg gcc cac ttc tgt acc 384
156 Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
157      100      105      110
158 agc ctc cag ggc ctg ctg ggc agc att gca ggt gtc atg gcg acg ctt 432
159 Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
160      115      120      125
161 ggc tac cca ctg ccc cag cct ctg cca ggg act gag cca gcc tgg gcc 480
162 Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
163      130      135      140
164 cct ggc cct gcc cac agt gac ttc ctc cag aag atg gat gac ttc tgg 528
165 Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
166      145      150      155
167 ctg ctg aag gag ctg cag acc tgg cta tgg cgt tca gcc aag gac ttc 576
168 Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
169      160      165      170      175
170 aac cgg ctt aag aag aag atg cag cct cca gca gct tca gtc acc ctg 624
171 Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
172      180      185      190
173 cac ttg gag gcc cat ggt ttc tga 648
174 His Leu Glu Ala His Gly Phe
175      195
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178 <211> LENGTH: 215
179 <212> TYPE: PRT
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181 <400> SEQUENCE: 4
182 Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
183      -15      -10      -5
184 Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
185      -1  1      5      10      15
186 Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
187      20      25      30
188 Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
189      35      40      45
190 Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
191      50      55      60
192 Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
193      65      70      75
194 Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
195      80      85      90      95

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196      Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
197                      100                      105                      110
198      Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
199                      115                      120                      125
200      Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
201                      130                      135                      140
202      Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
203                      145                      150                      155
204      Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
205                      160                      165                      170                      175
206      Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
207                      180                      185                      190
208      His Leu Glu Ala His Gly Phe
209                      195
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 203
213 <212> TYPE: PRT
214 <213> ORGANISM: rodent
215 <400> SEQUENCE: 5
216      Met Lys Val Leu Ala Ala Gly Ile Val Pro Leu Leu Leu Leu Val Leu
217          1          5          10          15
218      His Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn
219          20          25          30
220      Ala Thr Cys Ala Ile Arg His Pro Cys His Gly Asn Leu Met Asn Gln
221          35          40          45
222      Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe
223          50          55          60
224      Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu
225          65          70          75          80
226      Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn
227          85          90          95
228      Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr
229          100         105         110
230      Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
231          115         120         125
232      Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val
233          130         135         140
234      Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr
235          145         150         155         160
236      Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His Ser Asp Lys
237          165         170         175
238      Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr
239          180         185         190
240      Lys Gln Val Ile Ser Val Val Val Gln Ala Phe
241          195         200
243 <210> SEQ ID NO: 6
244 <211> LENGTH: 202
245 <212> TYPE: PRT
246 <213> ORGANISM: primate

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**VERIFICATION SUMMARY**

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